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RAW SEQUENCE LISTING   DATE: 05/08/2001
PATENT APPLICATION: US/09/674,824   TIME: 11:54:19

Input Set : A:\ES.txt
Output Set: N:\CRF3\05082001\I674824.raw

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     3 <110> APPLICANT: Lorz, et al
     5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT AND
     6       WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
     8 <130> FILE REFERENCE: AGR 1998/M 205/ FLH514413-3848
    10 <140> CURRENT APPLICATION NUMBER: 09/674,824
C--> 11 <141> CURRENT FILING DATE: 2000-02-16
    13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03156
    14 <151> PRIOR FILING DATE: 1999-05-07
    16 <150> PRIOR APPLICATION NUMBER: DE 198 20607.0
    17 <151> PRIOR FILING DATE: 1998-05-08
    19 <160> NUMBER OF SEQ ID NOS: 6
    21 <170> SOFTWARE: PatentIn version 3.0
    23 <210> SEQ ID NO: 1
    24 <211> LENGTH: 2771
    25 <212> TYPE: DNA
    26 <213> ORGANISM: Triticum aestivum
    28 <220> FEATURE:
    29 <221> NAME/KEY: CDS
    30 <222> LOCATION: (280)..(2547)
    32 <400> SEQUENCE: 1
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    35 accggctcat cacccatcac ctcggcctcg gccaccggca aacccccga tccgcttttg      120
    37 caggcagcgc actaaaaccc cggggagcgc gccccgcggc agcagcagca ccgcagtggg      180
    39 agagagaggc ttcgccccgg cccgcaccga gcggggcgat ccaccgtccg tgcgtccgca      240
    41 cctcctccgc ctcctcccct gtcccgcgcg cccacaccc atg gcg gcg acg ggc      294
    42                                                Met Ala Ala Thr Gly
    43                                                1               5
    45 gtc ggc gcc ggg tgc ctc gcc ccc agc gtc cgc ctg cgc gcc gat ccg      342
    46 Val Gly Ala Gly Cys Leu Ala Pro Ser Val Arg Leu Arg Ala Asp Pro
    47               10              15              20
    49 gcg acg gcg gcc cgg gcg tcc gcc tgc gtc gtc cgc gcg cgg ctc cgg      390
    50 Ala Thr Ala Ala Arg Ala Ser Ala Cys Val Val Arg Ala Arg Leu Arg
    51               25              30              35
    53 cgc ttg gcg cgg ggc cgc tac gtc gcc gag ctc agc agg gag ggc ccc      438
    54 Arg Leu Ala Arg Gly Arg Tyr Val Ala Glu Leu Ser Arg Glu Gly Pro
    55               40              45              50
    57 gcg gcg cgc ccc gcg cag cag cag caa ctg gcc ccg ccg ctc gtg cca      486
    58 Ala Ala Arg Pro Ala Gln Gln Gln Gln Leu Ala Pro Pro Leu Val Pro
    59       55              60              65
    61 ggc ttc ctc gcg ccg ccg ccg ccc gcg ccc gcc cag tcg ccg gcc ccg      534
    62 Gly Phe Leu Ala Pro Pro Pro Pro Ala Pro Ala Gln Ser Pro Ala Pro
    63 70              75              80              85
    65 acg cag ccg ccc ctg ccg gac gcc ggc gtg ggg gaa ctc gcg ccc gac      582
    66 Thr Gln Pro Pro Leu Pro Asp Ala Gly Val Gly Glu Leu Ala Pro Asp
    67               90              95              100
    69 ctc ctg ctc gaa ggg att gct gag gat tcc atc gac agc ata att gtg      630
    70 Leu Leu Leu Glu Gly Ile Ala Glu Asp Ser Ile Asp Ser Ile Ile Val
```

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71              105                     110                     115
73 gct gca agt gag cag gat tct gag atc atg gat gcg aat gag caa cct      678
74 Ala Ala Ser Glu Gln Asp Ser Glu Ile Met Asp Ala Asn Glu Gln Pro
75         120             125                     130
77 caa gct aaa gtt aca cgt agc atc gtg ttt gtg act ggt gaa gct gct      726
78 Gln Ala Lys Val Thr Arg Ser Ile Val Phe Val Thr Gly Glu Ala Ala
79     135                 140                     145
81 cct tat gca aag tca ggg ggg ttg gga gat gtt tgt ggt tcg tta cca      774
82 Pro Tyr Ala Lys Ser Gly Gly Leu Gly Asp Val Cys Gly Ser Leu Pro
83 150                 155                     160                 165
85 att gct ctt gct gct cgt ggt cac cga gtg atg gtt gta atg cca aga      822
86 Ile Ala Leu Ala Ala Arg Gly His Arg Val Met Val Val Met Pro Arg
87             170                 175                     180
89 tac tta aat ggg tcc tct gat aaa aac tat gca aag gca tta tac act      870
90 Tyr Leu Asn Gly Ser Ser Asp Lys Asn Tyr Ala Lys Ala Leu Tyr Thr
91             185                 190                     195
93 gcg aag cac att aag att cca tgc ttt ggg gga tca cat gaa gtg acc      918
94 Ala Lys His Ile Lys Ile Pro Cys Phe Gly Gly Ser His Glu Val Thr
95         200                 205                     210
97 ttt ttt cat gag tat aga gac aac gtc gat tgg gtg ttt gtc gat cat      966
98 Phe Phe His Glu Tyr Arg Asp Asn Val Asp Trp Val Phe Val Asp His
99     215                 220                     225
101 ccg tca tat cac aga cca gga agt tta tat gga gat aat ttt ggt gct     1014
102 Pro Ser Tyr His Arg Pro Gly Ser Leu Tyr Gly Asp Asn Phe Gly Ala
103 230                 235                     240                 245
105 ttt ggt gat aat cag ttc aga tac aca ctc ctt tgc tat gct gca tgc     1062
106 Phe Gly Asp Asn Gln Phe Arg Tyr Thr Leu Leu Cys Tyr Ala Ala Cys
107             250                 255                     260
109 gag gcc cca cta atc ctt gaa ttg gga gga tat att tat gga cag aat     1110
110 Glu Ala Pro Leu Ile Leu Glu Leu Gly Gly Tyr Ile Tyr Gly Gln Asn
111             265                 270                     275
113 tgc atg ttt gtt gtg aac gat tgg cat gcc agc ctt gtg cca gtc ctt     1158
114 Cys Met Phe Val Val Asn Asp Trp His Ala Ser Leu Val Pro Val Leu
115         280                 285                     290
117 ctt gct gca aaa tat aga cca tac ggt gtt tac aga gat tcc cgc agc     1206
118 Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr Arg Asp Ser Arg Ser
119     295                 300                     305
121 acc ctt gtt ata cat aat tta gca cat cag ggt gtg gag cct gca agt     1254
122 Thr Leu Val Ile His Asn Leu Ala His Gln Gly Val Glu Pro Ala Ser
123 310                 315                     320                 325
125 aca tat cct gat ctg gga ttg cct cct gaa tgg tat gga gct tta gaa     1302
126 Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp Tyr Gly Ala Leu Glu
127             330                 335                     340
129 tgg gta ttt cca gaa tgg gca agg agg cat gcc ctt gac aag ggt gag     1350
130 Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala Leu Asp Lys Gly Glu
131             345                 350                     355
133 gca gtt aac ttt ttg aaa gga gca gtt gtg aca gca gat cgg att gtg     1398
134 Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr Ala Asp Arg Ile Val
135             360                 365                     370
```

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137 acc gtc agt cag ggt tat tca tgg gag gtc aca act gct gaa ggt gga    1446
138 Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr Thr Ala Glu Gly Gly
139     375                 380                 385
141 cag ggc ctc aat gag ctc tta agc tcc cga aaa agt gta ttg aat gga    1494
142 Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys Ser Val Leu Asn Gly
143 390                 395                 400                 405
145 att gta aat gga att gac att aat gat tgg aac ccc acc aca gac aag    1542
146 Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn Pro Thr Thr Asp Lys
147                 410                 415                 420
149 tgt ctc cct cat cat tat tct gtc gat gac ctc tct gga aag gcc aaa    1590
150 Cys Leu Pro His His Tyr Ser Val Asp Asp Leu Ser Gly Lys Ala Lys
151             425                 430                 435
153 tgt aaa gct gaa ttg cag aag gag ttg ggt tta cct gta agg gag gat    1638
154 Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu Pro Val Arg Glu Asp
155         440                 445                 450
157 gtt cct ctg att ggc ttt att gga aga ctg gat tac cag aaa ggc att    1686
158 Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp Tyr Gln Lys Gly Ile
159     455                 460                 465
161 gat ctc att aaa atg gcc att cca gag ctc atg agg gag gac gtg caa    1734
162 Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met Arg Glu Asp Val Gln
163 470                 475                 480                 485
165 ttt gtc atg ctt gga tct ggg gat cca att ttt gaa ggc tgg atg aga    1782
166 Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe Glu Gly Trp Met Arg
167                 490                 495                 500
169 tct acc gag tcg agt tac aag gat aaa ttc cgt gga tgg gtt gga ttt    1830
170 Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg Gly Trp Val Gly Phe
171             505                 510                 515
173 agt gtt cca gtt tcc cac aga ata act gca ggt tgc gat ata ttg tta    1878
174 Ser Val Pro Val Ser His Arg Ile Thr Ala Gly Cys Asp Ile Leu Leu
175     520                 525                 530
177 atg cca tcg aga ttt gaa cct tgc ggt ctt aat cag cta tat gct atg    1926
178 Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Asn Gln Leu Tyr Ala Met
179     535                 540                 545
181 caa tat ggt aca gtt cct gta gtt cat gga act ggg ggc ctc cga gac    1974
182 Gln Tyr Gly Thr Val Pro Val Val His Gly Thr Gly Gly Leu Arg Asp
183 550                 555                 560                 565
185 aca gtc gag acc ttc aac cct ttt ggt gca aaa gga gag gag ggt aca    2022
186 Thr Val Glu Thr Phe Asn Pro Phe Gly Ala Lys Gly Glu Glu Gly Thr
187             570                 575                 580
189 ggg tgg gcg ttc tca ccg cta acc gtg gac aag atg ttg tgg gca ttg    2070
190 Gly Trp Ala Phe Ser Pro Leu Thr Val Asp Lys Met Leu Trp Ala Leu
191             585                 590                 595
193 cga acc gcg atg tcg aca ttc agg gag cac aag ccg tcc tgg gag ggg    2118
194 Arg Thr Ala Met Ser Thr Phe Arg Glu His Lys Pro Ser Trp Glu Gly
195         600                 605                 610
197 ctc atg aag cga ggc atg acg aaa gac cat acg tgg gac cat gcc ccg    2166
198 Leu Met Lys Arg Gly Met Thr Lys Asp His Thr Trp Asp His Ala Pro
199     615                 620                 625
201 agc agt acg agc aga tct tcg agt ggg cct tcg tgg acc aac cct acg    2214
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202 Ser Ser Thr Ser Arg Ser Ser Ser Gly Pro Ser Trp Thr Asn Pro Thr
203 630               635               640               645
205 tca tgt aga cgg gga ctg ggg agg tcc aag tgc gag tct cct tca gct     2262
206 Ser Cys Arg Arg Gly Leu Gly Arg Ser Lys Cys Glu Ser Pro Ser Ala
207               650               655               660
209 ctg aag aca tcc tct tca tcc ttc cgc ggc ccg gaa gga tac ccc tgt     2310
210 Leu Lys Thr Ser Ser Ser Ser Phe Arg Gly Pro Glu Gly Tyr Pro Cys
211               665               670               675
213 aca ttg cgt tgt cct gct aca gta gag tcg caa tgc gcc tgc ttg ctt     2358
214 Thr Leu Arg Cys Pro Ala Thr Val Glu Ser Gln Cys Ala Cys Leu Leu
215           680               685               690
217 tgg ttc gcc ggt tcg aga aca tat gac ggc tgt gct gct gcg gcg gtg     2406
218 Trp Phe Ala Gly Ser Arg Thr Tyr Asp Gly Cys Ala Ala Ala Ala Val
219     695               700               705
221 aca gct tcg ggt gga cga cag tta cag ttt tgg gga ata agg aag gga     2454
222 Thr Ala Ser Gly Gly Arg Gln Leu Gln Phe Trp Gly Ile Arg Lys Gly
223 710               715               720               725
225 tgt gct gca gga tgg tta aca gca aag cac cac tca gat ggc agc ctc     2502
226 Cys Ala Ala Gly Trp Leu Thr Ala Lys His His Ser Asp Gly Ser Leu
227               730               735               740
229 tct gtc cgt gtt aca gct gaa atc aga aac caa ctg gtg act ctt       2547
230 Ser Val Arg Val Thr Ala Glu Ile Arg Asn Gln Leu Val Thr Leu
231           745               750               755
233 tagccttagt gattgtgaag tttgttgcct tctgtgtatg ttgtcttgtc cttagctgac   2607
235 aaatatttga cctgttggag aattttatct ttgctgctgt ttttttttaa tcaaaagagg   2667
237 gggtttcctc cgatttcatt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   2727
239 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                   2771
242 <210> SEQ ID NO: 2
243 <211> LENGTH: 756
244 <212> TYPE: PRT
245 <213> ORGANISM: Triticum aestivum
247 <400> SEQUENCE: 2
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250 1               5               10               15
253 Leu Arg Ala Asp Pro Ala Thr Ala Ala Arg Ala Ser Ala Cys Val Val
254           20               25               30
257 Arg Ala Arg Leu Arg Arg Leu Ala Arg Gly Arg Tyr Val Ala Glu Leu
258           35               40               45
261 Ser Arg Glu Gly Pro Ala Ala Arg Pro Ala Gln Gln Gln Gln Leu Ala
262     50               55               60
265 Pro Pro Leu Val Pro Gly Phe Leu Ala Pro Pro Pro Ala Pro Ala
266 65               70               75               80
269 Gln Ser Pro Ala Pro Thr Gln Pro Pro Leu Pro Asp Ala Gly Val Gly
270               85               90               95
273 Glu Leu Ala Pro Asp Leu Leu Leu Glu Gly Ile Ala Glu Asp Ser Ile
274           100               105               110
277 Asp Ser Ile Ile Val Ala Ala Ser Glu Gln Asp Ser Glu Ile Met Asp
278           115               120               125
281 Ala Asn Glu Gln Pro Gln Ala Lys Val Thr Arg Ser Ile Val Phe Val
```

```
282      130                    135                    140
285 Thr Gly Glu Ala Ala Pro Tyr Ala Lys Ser Gly Gly Leu Gly Asp Val
286 145                    150                    155                    160
289 Cys Gly Ser Leu Pro Ile Ala Leu Ala Ala Arg Gly His Arg Val Met
290                    165                    170                    175
293 Val Val Met Pro Arg Tyr Leu Asn Gly Ser Ser Asp Lys Asn Tyr Ala
294                    180                    185                    190
297 Lys Ala Leu Tyr Thr Ala Lys His Ile Lys Ile Pro Cys Phe Gly Gly
298               195                    200                    205
301 Ser His Glu Val Thr Phe Phe His Glu Tyr Arg Asp Asn Val Asp Trp
302          210                    215                    220
305 Val Phe Val Asp His Pro Ser Tyr His Arg Pro Gly Ser Leu Tyr Gly
306 225                    230                    235                    240
309 Asp Asn Phe Gly Ala Phe Gly Asp Asn Gln Phe Arg Tyr Thr Leu Leu
310                    245                    250                    255
313 Cys Tyr Ala Ala Cys Glu Ala Pro Leu Ile Leu Glu Leu Gly Gly Tyr
314               260                    265                    270
317 Ile Tyr Gly Gln Asn Cys Met Phe Val Val Asn Asp Trp His Ala Ser
318          275                    280                    285
321 Leu Val Pro Val Leu Leu Ala Ala Lys Tyr Arg Pro Tyr Gly Val Tyr
322      290                    295                    300
325 Arg Asp Ser Arg Ser Thr Leu Val Ile His Asn Leu Ala His Gln Gly
326 305                    310                    315                    320
329 Val Glu Pro Ala Ser Thr Tyr Pro Asp Leu Gly Leu Pro Pro Glu Trp
330                    325                    330                    335
333 Tyr Gly Ala Leu Glu Trp Val Phe Pro Glu Trp Ala Arg Arg His Ala
334               340                    345                    350
337 Leu Asp Lys Gly Glu Ala Val Asn Phe Leu Lys Gly Ala Val Val Thr
338          355                    360                    365
341 Ala Asp Arg Ile Val Thr Val Ser Gln Gly Tyr Ser Trp Glu Val Thr
342      370                    375                    380
345 Thr Ala Glu Gly Gly Gln Gly Leu Asn Glu Leu Leu Ser Ser Arg Lys
346 385                    390                    395                    400
349 Ser Val Leu Asn Gly Ile Val Asn Gly Ile Asp Ile Asn Asp Trp Asn
350                    405                    410                    415
353 Pro Thr Thr Asp Lys Cys Leu Pro His His Tyr Ser Val Asp Asp Leu
354          420                    425                    430
357 Ser Gly Lys Ala Lys Cys Lys Ala Glu Leu Gln Lys Glu Leu Gly Leu
358          435                    440                    445
361 Pro Val Arg Glu Asp Val Pro Leu Ile Gly Phe Ile Gly Arg Leu Asp
362      450                    455                    460
365 Tyr Gln Lys Gly Ile Asp Leu Ile Lys Met Ala Ile Pro Glu Leu Met
366 465                    470                    475                    480
369 Arg Glu Asp Val Gln Phe Val Met Leu Gly Ser Gly Asp Pro Ile Phe
370                    485                    490                    495
373 Glu Gly Trp Met Arg Ser Thr Glu Ser Ser Tyr Lys Asp Lys Phe Arg
374               500                    505                    510
377 Gly Trp Val Gly Phe Ser Val Pro Val Ser His Arg Ile Thr Ala Gly
378          515                    520                    525
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VERIFICATION SUMMARY
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date